A Synthetic Protocell Model with a Self-Encoded System

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In all living systems, the genome is replicated by proteins encoded within the genome itself, which is an essential reaction for the sustentation and evolution in biological systems. To mimic such universal process, we constructed a simplified system comprised of a minimal set of biological components in which the genetic information is replicated by a self-encoded replicase. In this system, designated as the RNA–protein self-replication system, the catalytic subunit of replicase is synthesized from the template RNA that encodes itself, the replicase subsequently replicates the template RNA used for its own production.

This synthetic self-replicating system is one of the simplest systems available, consisting of just 144 gene products, which is comparable to the hypothetical minimal cell with approximately 150 gene products. It was further encapsulated within a microcompartment bounded by a lipid bilayer, so called liposome, resulting in a compartmentalized self-replicating system. The information and the function for its replication are encoded on different molecules and are compartmentalized into the microenvironment for evolvability. Successful construction of this in liposome self-replicating system shows a significant step toward synthetic life, as well as provides a further insight to the protomodel of cellular life.

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A Novel Evolution Concept of Protein Phosphorylation Mechanism

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Protein phosphorylation controls many cellular processes, but its mechanism is still a debatable subject, especially for protein kinases. According to the chemical property of N-phosphoamino acids, we deduce a novel three-step covalent mechanism (Ni et al., 2005), which is much different from 'in-line phosphorus transfer' mechanism (Valief et al., 2003).

It is known that human contains 518 kinds of protein kinases to regulate the cell's signal. Among them, more than 80% are the serine, threonine and tyrosine kinases with the hydroxyl group as the receptors phosphotransferases with a alcohol group as acceptor (E.C

2.7.1.X).While in the literature, there are phosphotransferases with a nitrogenous group as acceptor (E.C 2.7.3.X) and phosphotransferases with a carboxyl group as acceptor (E.C 2.7.2.X). Therefore, it might be a reasonable approach to illuminate the kinases catalyzing the phosphoryl transfer mechanism by comparison of these three types of kinases.

These three types of kinases, catalyze the γ-P of the ATP transfer to their corresponding substrates with three different phosphoryl groups of receptors, namely the HO-receptor, H_2N-receptor and the HOOC-receptor (see figure 1).

By the thermodynamical data, it seems that the carboxyl mixed anhydride **1**, easy to hydrolysis, contain much higher energy than the phosphoamide bond **2** (617 kJ mol^{-1}), which in turn is higher than the phosphoester bond **3** (597 kJ mol^{-1}) (Lange).

In this paper, by the evolution investigation, the Ser/Thr kinases phosphoryl transfer mechanism might go through the combination of the P-NH-residues and the P-OOC-residues mechanism. since the key catalytic residues of Ser/Thr kinases are Lys and Asp, it was proposed that the γ-P of the ATP is not directly transfer to the substrate, but might be proceeded by γ-P-Lys and γ-P-Asp high-energy intermediates and then finally phosphorylate the substrate.

E.C 2.7.2.X (phosphotransferases with a carboxyl group as acceptor)

1: **e.g** Carbamate kinase + ATP $\xrightarrow{\text{substrate}}$ sub–O–C(=O)–O–P(=O)(O$^-$)–O$^-$

1

E.C 2.7.3.X (phosphotransferases with a nitrogenous group as acceptor)

2: **e.g** Creatine kinase + ATP $\xrightarrow{\text{substrate}}$ sub–N(H)–P(=O)(O$^-$)–O$^-$

2

E.C 2.7.1.X (phosphotransferases with a alcohol group as acceptor).

3: **e.g** Serine kinase + ATP $\xrightarrow{\text{substrate}}$ sub–O–P(=O)(O$^-$)–O$^-$

3

figure 1

Lange's Chemistry Handbook Version 15th. section 4. properties of atoms, radicals, and bonds.

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